

## SEQUENCE LISTING

<110> OHARA, Osamu  
NAGASE, Takahiro  
OISHI, Michio  
YOKOTA, Hiroshi  
KAMIDA, Osamu

<120> Gene encoding a guanine nucleotide exchange factor and the gene product thereof

<130> 3190-100

<140> US Unassigned

<141> 2006-09-28

<150> PCT/JP2005/005918

<151> 2005-03-29

<150> JP P2004-106268

<151> 2004-03-31

<160> 27

<170> PatentIn version 3.1

<210> 1

<211> 4977

<212> DNA

<213> Homo sapiens

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<221> misc.feature

<223> Polynucleotide encoding the protein (SEQ ID NO:2) that have a function of guanine nucleotide exchange factor.

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<221> CDS

<222> (314)..(4336)

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<221> misc.feature

<222> (602)..(1126)

<223> A region encoding Dbl homology domain

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<222> (1202)..(1495)

<223> A region encoding Pleckstrin homology domain

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gcgcgtcccg agcccgcggg gcagctaccg ctgcaatctc cctgggggtgc cctccccagg	300
cagcaatgcc agg atg cct gtg tcc acc tcc ctg cac cag gat ggc agc	349
Met Pro Val Ser Thr Ser Leu His Gln Asp Gly Ser	
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cag gag cgg ccg gtg agc ctg acc tct acc acc tcc tcg tcg ggc tcc	397
Gln Glu Arg Pro Val Ser Leu Thr Ser Thr Thr Ser Ser Ser Gly Ser	
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tcc tgt gac agt cgc agt gcc atg gag gag ccc agc agc tcc gag gct	445
Ser Cys Asp Ser Arg Ser Ala Met Glu Glu Pro Ser Ser Ser Glu Ala	
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aac tcc gtg gcc gcc ctg acg gaa tgc atg cgg gac aag cag cag gcc 925  
Asn Ser Val Ala Ala Leu Thr Glu Cys Met Arg Asp Lys Gln Gln Ala  
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Lys Phe Phe Arg Asp Arg Gln Glu Leu Leu Gln His Ser Leu Pro Leu	
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Gly Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Leu Lys Tyr His Leu	
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ctg ctc cag gaa att gcc aaa cat ttt gat gaa gaa gag gat ggc ttt	1069
Leu Leu Gln Glu Ile Ala Lys His Phe Asp Glu Glu Glu Asp Gly Phe	
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Glu Val Val Glu Asp Ala Ile Asp Thr Met Thr Cys Val Ala Trp Tyr	
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Ile Asn Asp Met Lys Arg Arg His Glu His Ala Val Arg Leu Gln Glu	
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gaa agg acc ttt ttc ctc ttt gac aaa aca ctg ctt atc acc aag aag	1309
Glu Arg Thr Phe Phe Leu Phe Asp Lys Thr Leu Leu Ile Thr Lys Lys	
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gaa ggg gct acc cag gag gag gaa gag gaa gag gag gag gtg gtg gag 1837  
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 Val Ala Glu Gln Val Ala Asp Phe Ala Ser Ser Leu Leu Ala Ala Leu  
 560 565 570

cac tgc tgg cac tat cgg gcc aac gct tta ctt ttc tcc cgg ggc gct 2077  
 His Cys Trp His Tyr Arg Ala Asn Ala Leu Leu Phe Ser Arg Gly Ala  
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 Pro Ser Gly Arg Ser Pro Thr Ser Thr Glu Lys Arg Met Ser Phe Glu  
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 Ser Ile Ser Ser Leu Pro Glu Val Glu Pro Asp Pro Glu Ala Gly Ser  
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 Glu Gln Glu Val Phe Ser Ala Val Glu Gly Pro Ser Ala Glu Glu Thr  
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Pro Ser Asp Thr Glu Ser Pro Glu Val Leu Glu Thr Gln Leu Asp Ala	
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His Gln Gly Leu Leu Gly Met Asp Pro Pro Gly Asp Met Val Asp Phe	
670 675 680	
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Val Ala Ala Glu Ser Thr Glu Asp Leu Lys Ala Leu Ser Ser Glu Glu	
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Pro Ser Val Leu Asp Gln Ala Ser Val Ile Ala Glu Arg Phe Val Ser	
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Ala Thr Glu Asp Ser Pro Ser Val Asn Gly Met Glu Pro Pro Ser Pro	
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Gly Cys Pro Val Glu Pro Asp Arg Ser Ser Cys Lys Lys Lys Glu Ser	
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Ala Leu Ser Thr Arg Asp Arg Leu Leu Leu Asp Lys Ile Lys Ser Tyr	
830 835 840	
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Tyr Glu Asn Ala Glu His His Asp Ala Gly Phe Ser Val Arg Arg Arg	
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Glu Ser Leu Ser Tyr Ile Pro Lys Gly Leu Val Arg Asn Ser Ile Ser	
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Arg Phe Asn Ser Leu Pro Arg Pro Asp Pro Glu Pro Val Pro Pro Val	
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Ser Asp Ala Glu Phe Arg Pro Ser Ser Glu Ile Val Lys Ile Trp Glu	
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Gln Ala Asn Gly Phe Asp Leu His Glu Pro Leu Phe Ile Leu Glu Glu	
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cat gag ctg gga gcc atc aca gag gag tcg gcc act gcc tcc ccg gaa	3277
His Glu Leu Gly Ala Ile Thr Glu Glu Ser Ala Thr Ala Ser Pro Glu	
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Ser Ser Ser Pro Thr Glu Gly Arg Ser Pro Ala His Leu Ala Arg Glu	
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 Glu Asp Asn Arg Arg Val Ile Val Met Glu Lys Gly Pro Leu Pro  
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 agc ccc act gca ggg ctg gag gag agc agt ggc cag gga cca agc 4180  
 Ser Pro Thr Ala Gly Leu Glu Glu Ser Ser Gly Gln Gly Pro Ser  
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Gly Ala Gly Ser Leu Arg Ser Arg His Leu Pro Asn Ser Asn Asn Asn  
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Ser Ser Ser Trp Leu Asn Val Lys Gly Pro Leu Ser Pro Phe Asn Ser  
 65 70 75 80

Arg Ala Ala Ala Gly Pro Ala His His Lys Leu Ser Tyr Leu Gly Arg  
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Arg Ser Ile Val Glu Asp Tyr Leu Leu Lys Ile Ile Asp Thr Pro Gly  
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Leu Leu Lys Pro Glu Gln Val Ser Ala Leu Phe Gly Asn Ile Glu Asn  
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Ile Tyr Ala Leu Asn Ser Gln Leu Leu Arg Asp Leu Asp Ser Cys Asn  
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Phe Asp Ile Tyr Thr Gln Tyr Cys Asn Asn Tyr Pro Asn Ser Val Ala  
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Leu Glu Gly Thr Phe Arg Val His Arg Val Arg Asn Glu Arg Thr Phe  
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Phe Leu Phe Asp Lys Thr Leu Leu Ile Thr Lys Lys Arg Gly Asp His  
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Phe Val Tyr Lys Gly Asn Ile Pro Cys Ser Ser Leu Met Leu Ile Glu  
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Ser Thr Arg Asp Ser Leu Cys Phe Thr Val Thr His Tyr Lys His Ser  
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Lys Gln Gln Tyr Ser Ile Gln Ala Lys Thr Val Glu Glu Lys Arg Asn  
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Trp Thr His His Ile Lys Arg Leu Ile Leu Glu Asn His His Ala Thr  
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Pro Asn Arg Tyr Arg Cys Ser Pro Glu Arg Leu Lys Lys Ala Trp Ser  
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Glu Pro Thr Lys His Leu Leu Arg Gln Leu Asn Glu Lys Ala Arg Ala  
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Ala Gly Met Lys His Ala Gly Ser Ala Gly Thr Leu Leu Asp Phe Gly  
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Ser Pro Thr Ser Thr Glu Lys Arg Met Ser Phe Glu Ser Ile Ser Ser  
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Phe Ser Ala Val Glu Gly Pro Ser Ala Glu Glu Thr Pro Ser Asp Thr  
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Glu Ser Pro Glu Val Leu Glu Thr Gln Leu Asp Ala His Gln Gly Leu  
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Leu Gly Met Asp Pro Pro Gly Asp Met Val Asp Phe Val Ala Ala Glu  
 675 680 685

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Arg Ser Ser Val Ala Gln Glu Asp Ser Lys Ser Ser Gly Phe Gly Ser  
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Gln Leu Ser Pro Glu Val Asp Ile Ser Val Gly Val Ala Thr Glu Asp  
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835

840

845

Glu His His Asp Ala Gly Phe Ser Val Arg Arg Arg Glu Ser Leu Ser  
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Leu Pro Arg Pro Asp Pro Glu Pro Val Pro Pro Val Gly Ser Lys Arg  
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Pro Ser Gln Ala Val Lys Gly Asp Pro Pro Pro Ile Ser Asp Ala Glu  
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Phe Arg Pro Ser Ser Glu Ile Val Lys Ile Trp Glu Gly Met Glu Ser  
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Ser Gly Gly Ser Pro Gly Lys Gly Pro Gly Gln Gly Gln Ala Asn Gly  
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Phe Asp Leu His Glu Pro Leu Phe Ile Leu Glu Glu His Glu Leu Gly  
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Thr Glu Gly Arg Ser Pro Ala His Leu Ala Arg Glu Leu Lys Glu Leu  
 995 1000 1005

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1135

1140

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1150

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Pro Leu Ser Pro Thr Glu Thr Phe Ser Trp Pro Asp Val Arg Glu

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1165

1170

Leu Cys Ser Lys Tyr Ala Ser Arg Asp Glu Ala Arg Arg Ala Gly

1175

1180

1185

Gly Gly Arg Pro Arg Gly Pro Pro Val Asn Arg Ser His Ser Val

1190

1195

1200

Pro Glu Asn Met Val Glu Pro Pro Leu Ser Gly Arg Val Gly Arg

1205

1210

1215

Cys Arg Ser Leu Ser Thr Lys Arg Gly Arg Gly Gly Gly Glu Ala

1220

1225

1230

Ala Gln Ser Pro Gly Pro Leu Pro Gln Ser Lys Pro Asp Gly Gly

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Glu Thr Leu Tyr Val Thr Ala Asp Leu Thr Leu Glu Asp Asn Arg

1250

1255

1260

Arg Val Ile Val Met Glu Lys Gly Pro Leu Pro Ser Pro Thr Ala

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1270

1275

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<212> DNA

<213> Homo sapiens

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<221> misc\_feature

<223> A partial sequence of SEQ ID NO:1 consisting of the 581st to the 1675th nucleotides that comprises a region encoding Dbl homology domain and Pleckstrin homology domain, which encodes the amino acid sequence of SEQ ID NO:4.

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<222> (1)..(1095)

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 Lys Leu Ser Tyr Leu Gly Arg Val Val Arg Glu Ile Val Glu Thr Glu  
 1 5 10 15

cgc atg tac gla cag gac ctg cgc agc atc gtg gag gac tac ctc ttg 96  
 Arg Met Tyr Val Gln Asp Leu Arg Ser Ile Val Glu Asp Tyr Leu Leu  
 20 25 30

aag atc att gac aca ccc ggg ctg ctg aag cca gaa cag gtc agc gcc 144  
 Lys Ile Ile Asp Thr Pro Gly Leu Leu Lys Pro Glu Gln Val Ser Ala  
 35 40 45

ctc ttt ggg aac ata gaa aac atc tac gcg ctg aac agc cag ctc ctc 192  
 Leu Phe Gly Asn Ile Glu Asn Ile Tyr Ala Leu Asn Ser Gln Leu Leu  
 50 55 60

aga gac ctg gac agc tgc aat agt gac ccc gtg gct gtg gcc agc tgc 240  
 Arg Asp Leu Asp Ser Cys Asn Ser Asp Pro Val Ala Val Ala Ser Cys  
 65 70 75 80

ttt gtg gaa agg agc caa gag ttt got atc tac act cag tat tgc aac 288  
 Phe Val Glu Arg Ser Gln Glu Phe Asp Ile Tyr Thr Gln Tyr Cys Asn  
 85 90 95

aat tac ccc aac tcc gtg gcc gcc ctg acg gaa tgc atg cgg gac aag 336  
 Asn Tyr Pro Asn Ser Val Ala Ala Leu Thr Glu Cys Met Arg Asp Lys  
 100 105 110

cag cag gcc aag ttc ttt cgg gac cgg cag gag ctg cta cag cac tcg 384  
 Gln Gln Ala Lys Phe Phe Arg Asp Arg Gln Glu Leu Leu Gln His Ser  
 115 120 125

ctg ccc ttg ggc tcc tac ctg ctg aag cca gtc cag cgc atc ctc aag 432  
 Leu Pro Leu Gly Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Leu Lys  
 130 135 140

tac cac ctg ctg ctc cag gaa att gcc aaa cat ttt gat gaa gaa gag 480

aca gtg gag gag aaa cgg aac tgg act cac cac atc aag agg ctc atc 912  
Thr Val Glu Glu Lys Arg Asn Trp Thr His His Ile Lys Arg Leu Ile  
290 295 300

cta gag aac cac cat gcc acc att ccc cag aag gcc aag gaa gcc atc 960  
 Leu Glu Asn His His Ala Thr Ile Pro Gln Lys Ala Lys Glu Ala Ile  
 305 310 315 320

tig gaa atg gat tcc tat tat ccc aat cgg tac cgc tgc agc cca gag 1008  
 Leu Glu Met Asp Ser Tyr Tyr Pro Asn Arg Tyr Arg Cys Ser Pro Glu  
 325 330 335

cgg ctg aag aag gct tgg tcc tcc cag gat gag gtg tcc acc aat gtg 1056  
 Arg Leu Lys Lys Ala Trp Ser Ser Gln Asp Glu Val Ser Thr Asn Val  
 340 345 350

cgc cag ggg cgc cgg caa tct gag cca acc aaa cac ctg 1095  
 Arg Gln Gly Arg Arg Gln Ser Glu Pro Thr Lys His Leu  
 355 360 365

<210> 4

<211> 365

<212> PRT

<213> Homo sapiens

<400> 4

Lys Leu Ser Tyr Leu Gly Arg Val Val Arg Glu Ile Val Glu Thr Glu  
 1 5 10 15

Arg Met Tyr Val Gln Asp Leu Arg Ser Ile Val Glu Asp Tyr Leu Leu  
 20 25 30

Lys Ile Ile Asp Thr Pro Gly Leu Leu Lys Pro Glu Gln Val Ser Ala  
 35 40 45

Leu Phe Gly Asn Ile Glu Asn Ile Tyr Ala Leu Asn Ser Gln Leu Leu

50                      55                      60

Arg Asp Leu Asp Ser Cys Asn Ser Asp Pro Val Ala Val Ala Ser Cys  
65                      70                      75                      80

Phe Val Glu Arg Ser Gln Glu Phe Asp Ile Tyr Thr Gln Tyr Cys Asn  
                    85                      90                      95

Asn Tyr Pro Asn Ser Val Ala Ala Leu Thr Glu Cys Met Arg Asp Lys  
                    100                      105                      110

Gln Gln Ala Lys Phe Phe Arg Asp Arg Gln Glu Leu Leu Gln His Ser  
                    115                      120                      125

Leu Pro Leu Gly Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Leu Lys  
                    130                      135                      140

Tyr His Leu Leu Leu Gln Glu Ile Ala Lys His Phe Asp Glu Glu Glu  
145                      150                      155                      160

Asp Gly Phe Glu Val Val Glu Asp Ala Ile Asp Thr Met Thr Cys Val  
                    165                      170                      175

Ala Trp Tyr Ile Asn Asp Met Lys Arg Arg His Glu His Ala Val Arg  
                    180                      185                      190

Leu Gln Glu Ile Gln Ser Leu Leu Ile Asn Trp Lys Gly Pro Asp Leu  
                    195                      200                      205

Thr Thr Tyr Gly Glu Leu Val Leu Glu Gly Thr Phe Arg Val His Arg  
 210 215 220

Val Arg Asn Glu Arg Thr Phe Phe Leu Phe Asp Lys Thr Leu Leu Ile  
 225 230 235 240

Thr Lys Lys Arg Gly Asp His Phe Val Tyr Lys Gly Asn Ile Pro Cys  
 245 250 255

Ser Ser Leu Met Leu Ile Glu Ser Thr Arg Asp Ser Leu Cys Phe Thr  
 260 265 270

Val Thr His Tyr Lys His Ser Lys Gln Gln Tyr Ser Ile Gln Ala Lys  
 275 280 285

Thr Val Glu Glu Lys Arg Asn Trp Thr His His Ile Lys Arg Leu Ile  
 290 295 300

Leu Glu Asn His His Ala Thr Ile Pro Gln Lys Ala Lys Glu Ala Ile  
 305 310 315 320

Leu Glu Met Asp Ser Tyr Tyr Pro Asn Arg Tyr Arg Cys Ser Pro Glu  
 325 330 335

Arg Leu Lys Lys Ala Trp Ser Ser Gln Asp Glu Val Ser Thr Asn Val  
 340 345 350

Arg Gln Gly Arg Arg Gln Ser Glu Pro Thr Lys His Leu

355

360

365

&lt;210&gt; 5

&lt;211&gt; 1102

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

<223> Polynucleotide having kozak consensus sequence and methionine codon in its 5'-terminal, followed by partial sequence of SEQ ID NO:1 of the 581st to 1675th nucleotides having a region encoding Dbl homology domain and Pleckstrin homology domain, encoding SEQ ID NO:6.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (5)..(1102)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4)

&lt;223&gt; kozak consensus sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (5)..(7)

&lt;223&gt; methionine codon

&lt;400&gt; 5

cacc atg aag ctc agc tac ctg ggc cga gtg glg cgg gag atc gtg gag

49

Met Lys Leu Ser Tyr Leu Gly Arg Val Val Arg Glu Ile Val Glu

1

5

10

15

aca gag cgc atg tac gla cag gac ctg cgc agc atc gtg gag gac tac Thr Glu Arg Met Tyr Val Gln Asp Leu Arg Ser Ile Val Glu Asp Tyr 20 25 30	97
ctc ttg aag atc att gac aca ccc ggg ctg ctg aag cca gaa cag gtc Leu Leu Lys Ile Ile Asp Thr Pro Gly Leu Leu Lys Pro Glu Gln Val 35 40 45	145
agc gcc ctc ttt ggg aac ata gaa aac atc tac gcg ctg aac agc cag Ser Ala Leu Phe Gly Asn Ile Glu Asn Ile Tyr Ala Leu Asn Ser Gln 50 55 60	193
ctc ctc aga gac ctg gac agc tgc aat agt gac ccc gtg gct gtg gcc Leu Leu Arg Asp Leu Asp Ser Cys Asn Ser Asp Pro Val Ala Val Ala 65 70 75	241
agc tgc ttt gtg gaa agg agc caa gag ttt gat atc tac act cag tat Ser Cys Phe Val Glu Arg Ser Gln Glu Phe Asp Ile Tyr Thr Gln Tyr 80 85 90 95	289
tgc aac aat tac ccc aac tcc gtg gcc gcc ctg acg gaa tgc atg cgg Cys Asn Asn Tyr Pro Asn Ser Val Ala Ala Leu Thr Glu Cys Met Arg 100 105 110	337
gac aag cag cag gcc aag ttc ttt cgg gac cgg cag gag ctg cta cag Asp Lys Gln Gln Ala Lys Phe Phe Arg Asp Arg Gln Glu Leu Leu Gln 115 120 125	385
cac tcg ctg ccc ttg ggc tcc tac ctg ctg aag cca gtc cag cgc atc His Ser Leu Pro Leu Gly Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile 130 135 140	433
ctc aag tac cac ctg ctg ctc cag gaa att gcc aaa cat ttt gat gaa Leu Lys Tyr His Leu Leu Leu Gln Glu Ile Ala Lys His Phe Asp Glu 145 150 155	481
gaa gag gat ggc ttt gag gtg gtg gag gat gcc att gac acc atg acc	529

Glu Glu Asp Gly Phe	Glu Val Val Glu Asp Ala Ile	Asp Thr Met Thr	
160	165	170	175
tgt gtg gcc tgg tac atc aac gac atg aag agg agg cat gag cac gcg			577
Cys Val Ala Trp Tyr Ile Asn Asp Met Lys Arg Arg His Glu His Ala			
180	185	190	
gtc cgg ctg cag gag att cag tca ctc ctc atc aac tgg aag ggg ccc			625
Val Arg Leu Gln Glu Ile Gln Ser Leu Leu Ile Asn Trp Lys Gly Pro			
195	200	205	
gac ctg acc acc tac ggg gag ctt gtc ctg gag ggc aca ttc cgc gtg			673
Asp Leu Thr Thr Tyr Gly Glu Leu Val Leu Glu Gly Thr Phe Arg Val			
210	215	220	
cat cgc glg cgc aat gaa agg acc ttg ttc ctc ttg gac aaa aca ctg			721
His Arg Val Arg Asn Glu Arg Thr Phe Phe Leu Phe Asp Lys Thr Leu			
225	230	235	
ctt atc acc aag aag cgg ggc gat cac ttg gtc tac aag ggc aac atc			769
Leu Ile Thr Lys Lys Arg Gly Asp His Phe Val Tyr Lys Gly Asn Ile			
240	245	250	255
cgg tgc tcc tcc ctg atg ctg atc gaa agc acc aga gac tcc ctg tgc			817
Pro Cys Ser Ser Leu Met Leu Ile Glu Ser Thr Arg Asp Ser Leu Cys			
260	265	270	
ttc act gtc acc cac tac aag cac agc aag cag cag tac agc atc cag			865
Phe Thr Val Thr His Tyr Lys His Ser Lys Gln Gln Tyr Ser Ile Gln			
275	280	285	
gcc aag aca gtg gag gag aca cgg aac tgg act cac cac atc aag agg			913
Ala Lys Thr Val Glu Glu Lys Arg Asn Trp Thr His His Ile Lys Arg			
290	295	300	
ctc atc cta gag aac cac cat gcc acc att ccc cag aag gcc aag gaa			961
Leu Ile Leu Glu Asn His His Ala Thr Ile Pro Gln Lys Ala Lys Glu			
305	310	315	

gcc atc ttg gaa atg gat tcc tat tat ccc aat cgg tac cgc tgc agc 1009  
 Ala Ile Leu Glu Met Asp Ser Tyr Tyr Pro Asn Arg Tyr Arg Cys Ser  
 320 325 330 335

cca gag cgg ctg aag aag gct tgg tcc tcc cag gat gag gtg tcc acc 1057  
 Pro Glu Arg Leu Lys Lys Ala Trp Ser Ser Gln Asp Glu Val Ser Thr  
 340 345 350

aat gtg cgc cag ggg cgc cgg cca tct gag cca acc aaa cac ctg 1102  
 Asn Val Arg Gln Gly Arg Arg Gln Ser Glu Pro Thr Lys His Leu  
 355 360 365

<210> 6

<211> 366

<212> PRT

<213> Homo sapiens

<400> 6

Met Lys Leu Ser Tyr Leu Gly Arg Val Val Arg Glu Ile Val Glu Thr  
 1 5 10 15

Glu Arg Met Tyr Val Gln Asp Leu Arg Ser Ile Val Glu Asp Tyr Leu  
 20 25 30

Leu Lys Ile Ile Asp Thr Pro Gly Leu Leu Lys Pro Glu Gln Val Ser  
 35 40 45

Ala Leu Phe Gly Asn Ile Glu Asn Ile Tyr Ala Leu Asn Ser Gln Leu  
 50 55 60

Leu Arg Asp Leu Asp Ser Cys Asn Ser Asp Pro Val Ala Val Ala Ser

65                      70                      75                      80

Cys Phe Val Glu Arg Ser Gln Glu Phe Asp Ile Tyr Thr Gln Tyr Cys  
                                  85                      90                      95

Asn Asn Tyr Pro Asn Ser Val Ala Ala Leu Thr Glu Cys Met Arg Asp  
                                  100                      105                      110

Lys Gln Gln Ala Lys Phe Phe Arg Asp Arg Gln Glu Leu Leu Gln His  
                                  115                      120                      125

Ser Leu Pro Leu Gly Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Leu  
                                  130                      135                      140

Lys Tyr His Leu Leu Leu Gln Glu Ile Ala Lys His Phe Asp Glu Glu  
                                  145                      150                      155                      160

Glu Asp Gly Phe Glu Val Val Glu Asp Ala Ile Asp Thr Met Thr Cys  
                                  165                      170                      175

Val Ala Trp Tyr Ile Asn Asp Met Lys Arg Arg His Glu His Ala Val  
                                  180                      185                      190

Arg Leu Gln Glu Ile Gln Ser Leu Leu Ile Asn Trp Lys Gly Pro Asp  
                                  195                      200                      205

Leu Thr Thr Tyr Gly Glu Leu Val Leu Glu Gly Thr Phe Arg Val His  
                                  210                      215                      220

Arg Val Arg Asn Glu Arg Thr Phe Phe Leu Phe Asp Lys Thr Leu Leu  
 225 230 235 240

Ile Thr Lys Lys Arg Gly Asp His Phe Val Tyr Lys Gly Asn Ile Pro  
 245 250 255

Cys Ser Ser Leu Met Leu Ile Glu Ser Thr Arg Asp Ser Leu Cys Phe  
 260 265 270

Thr Val Thr His Tyr Lys His Ser Lys Gln Gln Tyr Ser Ile Gln Ala  
 275 280 285

Lys Thr Val Glu Glu Lys Arg Asn Trp Thr His His Ile Lys Arg Leu  
 290 295 300

Ile Leu Glu Asn His His Ala Thr Ile Pro Gln Lys Ala Lys Glu Ala  
 305 310 315 320

Ile Leu Glu Met Asp Ser Tyr Tyr Pro Asn Arg Tyr Arg Cys Ser Pro  
 325 330 335

Glu Arg Leu Lys Lys Ala Trp Ser Ser Gln Asp Glu Val Ser Thr Asn  
 340 345 350

Val Arg Gln Gly Arg Arg Gln Ser Glu Pro Thr Lys His Leu  
 355 360 365

<210> 7

<211> 22

<212> DNA

<213> Artificial

<220>

<223> Designed polynucleotide based on the sequence of SEQ ID NO:1 for use as a primer

<400> 7

gggagatgtc accacagcgt tt

22

<210> 8

<211> 29

<212> DNA

<213> Artificial

<220>

<223> Designed polynucleotide based on the sequence of SEQ ID NO:1 for use as a primer

<400> 8

aatggatccc gaccgacaga gttcaaggc

29

<210> 9

<211> 34

<212> DNA

<213> Artificial

<220>

<223> Designed polynucleotide based on the sequence of SEQ ID NO:1 for use as a primer

<400> 9

cacctgaag ctacgtacc tgggccgagt ggtg

34

<210> 10

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Designed polynucleotide based on the sequence of SEQ ID NO:1 for use as a primer

<400> 10

caggtgittg gttggctcag attgcc

26

<210> 11

<211> 35

<212> DNA

<213> Artificial

<220>

<223> Designed polynucleotide based on the sequence of proto-Dbl for use as a primer

<400> 11

aatagatctg gaaatggcag ttttaagaa ccacg

35

<210> 12

<211> 29

<212> DNA

<213> Artificial

<220>

<223> Designed polynucleotide based on the sequence of proto-Dbl for use as a primer

<400> 12

aaigtgcacc tgcctcaaca aaatatlcc

29

<210> 13

<211> 29

<212> DNA

<213> Artificial

<220>

<223> Designed polynucleotide based on the sequence of Cdc42 for use as a primer

<400> 13

caccatgcag acaattaagt gtgtgttg

29

<210> 14

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Designed polynucleotide based on the sequence of Cdc42 for use as a primer

<400> 14

tcatgcagc acacacctgc ggctc

25

<210> 15

<211> 29

<212> DNA

<213> Artificial

<220>

<223> Designed polynucleotide based on the sequence of RhoA for use as a primer

<400> 15

caccatggct gccatccgga agaaactgg

29

<210> 16  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<223> Designed polynucleotide based on the sequence of RhoA for use as  
a primer

<400> 16  
tcacoagaca aggcaaccag attttttc 28

<210> 17  
<211> 29  
<212> DNA  
<213> Artificial

<220>  
<223> Designed polynucleotide based on the sequence of Rac1 for use as  
a primer

<400> 17  
caccatgcag gccatcaagt gtgtggtgg 29

<210> 18  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<223> Designed polynucleotide based on the sequence of Rac1 for use as  
a primer

<400> 18

ttacaacagc aggcatttcc tcttcc 26

<210> 19

<211> 7

<212> DNA

<213> artificial

<220>

<223> Designed oligonucleotide including Kozak consensus sequence followed by a methionine codon.

<400> 19

caccatg 7

<210> 20

<211> 576

<212> DNA

<213> homo sapiens

<220>

<221> misc\_feature

<223> Cdc42 gene

<400> 20

atgcagacaa ttaagtgigt tgttgtggc gaiggtgctg ttggtaaaac atgtctcctg 60

atatcttaca caacaaccaa atttccatcg gaatatgtac cgactgtttt tgacaactat 120

gcagtcacag ttatgattgg tggagaacca tatactcttg gactttttga tactgcaggg 180

caagaggatt atgcagatt acgaccgctg agttatccac aaacagatgt atttctagtc 240

tgttttcag tggctctcc atcttcattt gaaaacgtga aagaaaagtg ggtgcctgag 300

ataactcacc actgtccaaa gactccttcc ttgcttgttg ggactcaaat tgatctcaga 360

gatgaccct ctactattga gaaacttgc aagaacaaac agaagcctat cactccagag 420

actgtgaaa agctggcccg tgacctgaag gctgtcaagt atgtggagtg ttctgcactt 480

acacagaaag gcctaagaa tglatttgac gaagcaatat tggctgccct ggagcctcca 540

gaaccgaaga agagccgcag gtgtgtgtg ctatga 576

<210> 21

<211> 191

<212> PRT

<213> homo sapiens

<220>

<221> misc\_feature

<223> Cdc42

<400> 21

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys

1 5 10 15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser Glu Tyr

20 25 30

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile Gly Gly

35 40 45

Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu Asp Tyr

50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Val  
 65 70 75 80

Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys Glu Lys  
 85 90 95

Trp Val Pro Glu Ile Thr His His Cys Pro Lys Thr Pro Phe Leu Leu  
 100 105 110

Val Gly Thr Gln Ile Asp Leu Arg Asp Asp Pro Ser Thr Ile Glu Lys  
 115 120 125

Leu Ala Lys Asn Lys Gln Lys Pro Ile Thr Pro Glu Thr Ala Glu Lys  
 130 135 140

Leu Ala Arg Asp Leu Lys Ala Val Lys Tyr Val Glu Cys Ser Ala Leu  
 145 150 155 160

Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu Ala Ala  
 165 170 175

Leu Glu Pro Pro Glu Pro Lys Lys Ser Arg Arg Cys Val Leu Leu  
 180 185 190

<210> 22

<211> 582

<212> DNA

<213> homo sapiens

<220>

<221> misc\_feature

<223> RhoA gene

<400> 22

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atggctgcca tccggaagaa actggtgatt gttggtgatg gagcctgtgg aaagacatgc    60
ttgtctatag tcttcagcaa ggaccagttc ccagagggtg atgtgccac agtgtttgag    120
aactaigtgg cagatatcga ggtgatgga aagcaggtag agttggcttt gtgggacaca    180
gctgggcagg aagattatga tcgcctgagg cccctcctc acccagatac cgatgttata    240
ctgatgtgtt ttccatcga cagccctgat agtttagaaa acatcccaga aaagtggaac    300
ccagaagtca agcatttctg tcccaacgtg cccatcatcc tggttgggaa taagaaggat    360
cttcggaatg atgagcacac aaggcgggag ctagccaaga tgaagcagga gccggtgaaa    420
cctgaagaag gcagagatat ggcaaacagg attggcgctt ttgggtacat ggagtgttca    480
gcaaaagacca aagatggagt gagagagggt ttgaaatgg ctacgagagc tgctctgcaa    540
gctagacgtg ggaagaaaaa atctggttgc ctgtcttgt ga                    582

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<210> 23

<211> 193

<212> PRT

<213> homo sapiens

<220>

<221> misc\_feature

<223> RhoA

<400> 23

Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly Ala Cys  
 1 5 10 15

Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Lys Asp Gln Phe Pro Glu  
 20 25 30

Val Tyr Val Pro Thr Val Phe Glu Asn Tyr Val Ala Asp Ile Glu Val  
 35 40 45

Asp Gly Lys Gln Val Glu Leu Ala Leu Trp Asp Thr Ala Gly Gln Glu  
 50 55 60

Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Asp Thr Asp Val Ile  
 65 70 75 80

Leu Met Cys Phe Ser Ile Asp Ser Pro Asp Ser Leu Glu Asn Ile Pro  
 85 90 95

Glu Lys Trp Thr Pro Glu Val Lys His Phe Cys Pro Asn Val Pro Ile  
 100 105 110

Ile Leu Val Gly Asn Lys Lys Asp Leu Arg Asn Asp Glu His Thr Arg  
 115 120 125

Arg Glu Leu Ala Lys Met Lys Gln Glu Pro Val Lys Pro Glu Glu Gly  
 130 135 140

Arg Asp Met Ala Asn Arg Ile Gly Ala Phe Gly Tyr Met Glu Cys Ser  
 145 150 155 160

Ala Lys Thr Lys Asp Gly Val Arg Glu Val Phe Glu Met Ala Thr Arg  
 165 170 175

Ala Ala Leu Gln Ala Arg Arg Gly Lys Lys Lys Ser Gly Cys Leu Val  
 180 185 190

Leu

<210> 24  
 <211> 579  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> misc\_feature  
 <223> Rac1 gene

<400> 24  
 atgcaggcca tcaagtgtgt ggtggtggga gacggagctg taggtaaaac ttgcctactg 60  
 atcagttaca caaccaatgc atttcctgga gaatatatcc ctactgtcct tgacaattat 120  
 tctgccaatg ttatggtaga tggaaaaccg gtgaatctgg gcttatggga tacagctgga 180  
 caagaagatt atgacagatt acgcccccta tctatccgc aaacagatgt gttcttaatt 240  
 tgcttttccc ttgtgagtc tgcattatct gaaaatgtcc gtgcaaagtg gtatcctgag 300  
 gtgcggcacc acgtgccaa cactcccatc atcctagtgg gaactaaact tgatcttagg 360  
 gatgataaag acacgatcga gaaactgaag gagaagaagc tgactcccat cacctatccg 420

cagggtcag ccatggctaa ggagattggt gctgtaaaat acctggagtg ctcggcgctc 480  
 acacagcgag gccacaagac agtgtttgac gaagcgatcc gagcagtcct ctgcccgctt 540  
 cccgtgaaga agaggaagag aaaaatgcctg ctgtttgtaa 579

<210> 25  
 <211> 192  
 <212> PRT  
 <213> homo sapiens

<220>  
 <221> misc\_feature  
 <223> Rac1

<400> 25

Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys  
 1 5 10 15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly Glu Tyr  
 20 25 30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val Asp Gly  
 35 40 45

Lys Pro Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr  
 50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Ile  
 65 70 75 80

Cys Phe Ser Leu Val Ser Pro Ala Ser Phe Glu Asn Val Arg Ala Lys  
                     85                    90                    95

Trp Tyr Pro Glu Val Arg His His Cys Pro Asn Thr Pro Ile Ile Leu  
                     100                    105                    110

Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Asp Thr Ile Glu Lys  
                     115                    120                    125

Leu Lys Glu Lys Lys Leu Thr Pro Ile Thr Tyr Pro Gln Gly Leu Ala  
                     130                    135                    140

Met Ala Lys Glu Ile Gly Ala Val Lys Tyr Leu Glu Cys Ser Ala Leu  
 145                    150                    155                    160

Thr Gln Arg Gly Leu Lys Thr Val Phe Asp Glu Ala Ile Arg Ala Val  
                     165                    170                    175

Leu Cys Pro Pro Pro Val Lys Lys Arg Lys Arg Lys Cys Leu Leu Leu  
                     180                    185                    190

<210> 26

<211> 3652

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Gene encoding proto-Dbl (SEQ ID NO:27)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (175)..(2952)

&lt;400&gt; 26

tttttttt ttctcccaa cattgctgcc actgtgctaa tgggaagcacc acggcagctt 60

tglttgatag agatttttgg ctgccgtttt taaatactac ccaagaagca gctcgtatit 120

catcaatglt gcgttgacaa ttggaaaaga aaagtgtaat tgcgtacagg cgaa atg 177  
Met  
1

gca gaa gca aat ccc cgg aga ggc aag atg agg ttc aga agg aat gcg 225  
Ala Glu Ala Asn Pro Arg Arg Gly Lys Met Arg Phe Arg Arg Asn Ala  
5 10 15

gct tcc ttc cct ggg aac ttg cac ttg gtt ttg git tta cgt cct acc 273  
Ala Ser Phe Pro Gly Asn Leu His Leu Val Leu Val Leu Arg Pro Thr  
20 25 30

agc ttt ctt caa cga acg ttc aca gac att gga ttt tgg ttt agt cag 321  
Ser Phe Leu Gln Arg Thr Phe Thr Asp Ile Gly Phe Trp Phe Ser Gln  
35 40 45

gag gat ttt atg cct aaa tta cca gtt gtt atg ctg agc tca gtt agt 369  
Glu Asp Phe Met Pro Lys Leu Pro Val Val Met Leu Ser Ser Val Ser  
50 55 60 65

gat ttg ctg aca tac att gat gac aag caa tta acc cct gag tta ggc 417  
Asp Leu Leu Thr Tyr Ile Asp Asp Lys Gln Leu Thr Pro Glu Leu Gly  
70 75 80

ggc acc ttg cag tac tgc cac agt gaa tgg aic atc ttc aga aat gct 465  
Gly Thr Leu Gln Tyr Cys His Ser Glu Trp Ile Ile Phe Arg Asn Ala

85	90	95	
ata gaa aat ttt gcc ctc aca gtg aaa gaa atg gct cag atg tta cag			513
Ile Glu Asn Phe Ala Leu Thr Val Lys Glu Met Ala Gln Met Leu Gln			
100	105	110	
tcc ttt gga act gaa ctg gct gag aca gaa cta cca gat gat att ccc			561
Ser Phe Gly Thr Glu Leu Ala Glu Thr Glu Leu Pro Asp Asp Ile Pro			
115	120	125	
tca ata gaa gaa att ctg gca att cgt gct gaa agg tat cat ctg ttg			609
Ser Ile Glu Glu Ile Leu Ala Ile Arg Ala Glu Arg Tyr His Leu Leu			
130	135	140	145
aag aat gat att aca gct gta acc aaa gaa gga aaa att ctg cta aca			657
Lys Asn Asp Ile Thr Ala Val Thr Lys Glu Gly Lys Ile Leu Leu Thr			
150	155	160	
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Asn Leu Glu Val Pro Asp Thr Glu Gly Ala Val Ser Ser Arg Leu Glu			
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Cys His Arg Gln Ile Ser Gly Asp Trp Gln Thr Ile Asn Lys Leu Leu			
180	185	190	
act caa gta cat gat atg gaa aca gct ttt gat gga ttt tgg gaa aaa			801
Thr Gln Val His Asp Met Glu Thr Ala Phe Asp Gly Phe Trp Glu Lys			
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cat caa tta aaa atg gag cag tat ctg caa cta tgg aag ttt gag cag			849
His Gln Leu Lys Met Glu Gln Tyr Leu Gln Leu Trp Lys Phe Glu Gln			
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gat ttt caa cag ctt gtg act gaa gtt gaa ttt cta tta aac caa caa			897
Asp Phe Gln Gln Leu Val Thr Glu Val Glu Phe Leu Leu Asn Gln Gln			
230	235	240	

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Ala Glu Leu Ala Asp Val Thr Gly Thr Ile Ala Gln Val Lys Gln Lys	
245 250 255	
ata aaa aaa ttg gaa aac tta gat gaa aat tct cog gag cta tta tca	993
Ile Lys Lys Leu Glu Asn Leu Asp Glu Asn Ser Gln Glu Leu Leu Ser	
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Lys Ala Gln Phe Val Ile Leu His Gly His Lys Leu Ala Ala Asn His	
275 280 285	
cat tat gca ctt gat tta atc tgc cag agg tgc aat gag cta cgt tac	1089
His Tyr Ala Leu Asp Leu Ile Cys Gln Arg Cys Asn Glu Leu Arg Tyr	
290 295 300 305	
ctt tct gat att ttg gtt aat gag ata aaa gca aaa cgg ata caa ctc	1137
Leu Ser Asp Ile Leu Val Asn Glu Ile Lys Ala Lys Arg Ile Gln Leu	
310 315 320	
agc agg acc ttc aaa atg cat aaa ctc cta cag cag gct cgt caa tgc	1185
Ser Arg Thr Phe Lys Met His Lys Leu Leu Gln Gln Ala Arg Gln Cys	
325 330 335	
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Cys Asp Glu Gly Glu Cys Leu Ala Asn Gln Glu Ile Asp Lys Phe	
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Gln Ser Lys Glu Asp Ala Gln Lys Ala Leu Gln Asp Ile Glu Asn Phe	
355 360 365	
ctt gaa atg gct cta ccc ttt ata aat tat gaa cct gaa aca ctg cag	1329
Leu Glu Met Ala Leu Pro Phe Ile Asn Tyr Glu Pro Glu Thr Leu Gln	
370 375 380 385	
tat gaa ttt gat gta ata tta tct cct gag ctt aag gtt caa atg aag	1377
Tyr Glu Phe Asp Val Ile Leu Ser Pro Glu Leu Lys Val Gln Met Lys	

390	395	400	
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Thr Ile Gln Leu Lys Leu Glu Asn Ile Arg Ser Ile Phe Glu Asn Gln			
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cag gct ggt ttc agg aac ctg gca gat aag cat gtg agg cca atc caa			1473
Gln Ala Gly Phe Arg Asn Leu Ala Asp Lys His Val Arg Pro Ile Gln			
420	425	430	
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Phe Val Val Pro Thr Pro Glu Asn Leu Val Thr Ser Gly Thr Pro Phe			
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Phe Ser Ser Lys Gln Gly Lys Lys Thr Trp Arg Gln Asn Gln Ser Asn			
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tta aaa att gaa gtg gtg cct gat tgt cag gag aag aga agt tct ggt			1617
Leu Lys Ile Glu Val Val Pro Asp Cys Gln Glu Lys Arg Ser Ser Gly			
470	475	480	
cca tcc tcc agt ttg gac aat ggc aat agc ttg gat gtt tta aag aac			1665
Pro Ser Ser Ser Leu Asp Asn Gly Asn Ser Leu Asp Val Leu Lys Asn			
485	490	495	
cac gta cta aat gaa ctg ata cag act gag aga gtt tat gtt cga gaa			1713
His Val Leu Asn Glu Leu Ile Gln Thr Glu Arg Val Tyr Val Arg Glu			
500	505	510	
ctg tat act gtt ttg ttg ggt tat aga gcg gag atg gat aat cca gag			1761
Leu Tyr Thr Val Leu Leu Gly Tyr Arg Ala Glu Met Asp Asn Pro Glu			
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atg ttt gat ctt atg cca cct ctc ctg aga aat aaa aag gac att ctc			1809
Met Phe Asp Leu Met Pro Pro Leu Leu Arg Asn Lys Lys Asp Ile Leu			
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Phe Gly Asn Met Ala Glu Ile Tyr Glu Phe His Asn Asp Ile Phe Leu	
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Ser Ser Leu Glu Asn Cys Ala His Ala Pro Glu Arg Val Gly Pro Cys	
565 570 575	
ttc ctg gaa agg aag gat gat ttt cag atg tat gca aaa tai tgt cag	1953
Phe Leu Glu Arg Lys Asp Asp Phe Gln Met Tyr Ala Lys Tyr Cys Gln	
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Asn Lys Pro Arg Ser Glu Thr Ile Trp Arg Lys Tyr Ser Glu Cys Ala	
595 600 605	
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Phe Phe Gln Glu Cys Gln Arg Lys Leu Lys His Arg Leu Arg Leu Asp	
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Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Thr Lys Tyr Gln Leu Leu	
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Leu Lys Glu Leu Leu Lys Tyr Ser Lys Asp Cys Glu Gly Ser Ala Leu	
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Leu Lys Lys Ala Leu Asp Ala Met Leu Asp Leu Leu Lys Ser Val Asn	
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Asp Ser Met His Gln Ile Ala Ile Asn Gly Tyr Ile Gly Asn Leu Asn	
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gaa ctg ggc aag atg ata atg caa ggt gga ttc agc gtt tgg ata ggg	2289
Glu Leu Gly Lys Met Ile Met Gln Gly Gly Phe Ser Val Trp Ile Gly	

690	695	700	705	
cac aag aaa ggt gct aca aaa atg aag gat ttg gct aga ttc aaa cca				2337
His Lys Lys Gly Ala Thr Lys Met Lys Asp Leu Ala Arg Phe Lys Pro				
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atg cag cga cac ctt ttc ttg tat gaa aaa gcc att gtt ttt tgc aaa				2385
Met Gln Arg His Leu Phe Leu Tyr Glu Lys Ala Ile Val Phe Cys Lys				
	725	730	735	
agg cgt gtt gaa agt gga gaa ggc tct gac aga tac ccg tca tac agt				2433
Arg Arg Val Glu Ser Gly Glu Gly Ser Asp Arg Tyr Pro Ser Tyr Ser				
	740	745	750	
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Phe Lys His Cys Trp Lys Met Asp Glu Val Gly Ile Thr Glu Tyr Val				
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Lys Gly Asp Asn Arg Lys Phe Glu Ile Trp Tyr Gly Glu Lys Glu Glu				
	770	775	780	785
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Val Tyr Ile Val Gln Ala Ser Asn Val Asp Val Lys Met Thr Trp Leu				
	790	795	800	
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Lys Lys Arg Lys Gln Gln Asp Gln Leu Thr Glu Arg Asp Lys Phe Gln				
	820	825	830	
att tct ctt cag cag aat gat gaa aag caa cag gga gct ttt ata agt				2721
Ile Ser Leu Gln Gln Asn Asp Glu Lys Gln Gln Gly Ala Phe Ile Ser				
	835	840	845	

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 850 855 860 865

gag gca att gcg tca gtt cag gca gaa gca aat aca gtt tgg act gag 2817  
 Glu Ala Ile Ala Ser Val Gln Ala Glu Ala Asn Thr Val Trp Thr Glu  
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 915 920 925

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35 40 45

Gln Glu Asp Phe Met Pro Lys Leu Pro Val Val Met Leu Ser Ser Val  
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Ser Asp Leu Leu Thr Tyr Ile Asp Asp Lys Gln Leu Thr Pro Glu Leu  
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Gly Gly Thr Leu Gln Tyr Cys His Ser Glu Trp Ile Ile Phe Arg Asn  
85 90 95

Ala Ile Glu Asn Phe Ala Leu Thr Val Lys Glu Met Ala Gln Met Leu  
100 105 110

Gln Ser Phe Gly Thr Glu Leu Ala Glu Thr Glu Leu Pro Asp Asp Ile  
115 120 125

Pro Ser Ile Glu Glu Ile Leu Ala Ile Arg Ala Glu Arg Tyr His Leu  
130 135 140

Leu Lys Asn Asp Ile Thr Ala Val Thr Lys Glu Gly Lys Ile Leu Leu  
145 150 155 160

Thr Asn Leu Glu Val Pro Asp Thr Glu Gly Ala Val Ser Ser Arg Leu  
165 170 175

Glu Cys His Arg Gln Ile Ser Gly Asp Trp Gln Thr Ile Asn Lys Leu  
180 185 190

Leu Thr Gln Val His Asp Met Glu Thr Ala Phe Asp Gly Phe Trp Glu  
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Lys His Gln Leu Lys Met Glu Gln Tyr Leu Gln Leu Trp Lys Phe Glu  
210 215 220

Gln Asp Phe Gln Gln Leu Val Thr Glu Val Glu Phe Leu Leu Asn Gln  
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Gln Ala Glu Leu Ala Asp Val Thr Gly Thr Ile Ala Gln Val Lys Gln  
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Lys Ile Lys Lys Leu Glu Asn Leu Asp Glu Asn Ser Gln Glu Leu Leu  
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Ser Lys Ala Gln Phe Val Ile Leu His Gly His Lys Leu Ala Ala Asn  
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His His Tyr Ala Leu Asp Leu Ile Cys Gln Arg Cys Asn Glu Leu Arg  
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Tyr Leu Ser Asp Ile Leu Val Asn Glu Ile Lys Ala Lys Arg Ile Gln  
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Leu Ser Arg Thr Phe Lys Met His Lys Leu Leu Gln Gln Ala Arg Gln  
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Cys Cys Asp Glu Gly Glu Cys Leu Leu Ala Asn Gln Glu Ile Asp Lys  
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Phe Gln Ser Lys Glu Asp Ala Gln Lys Ala Leu Gln Asp Ile Glu Asn  
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Phe Leu Glu Met Ala Leu Pro Phe Ile Asn Tyr Glu Pro Glu Thr Leu  
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Gln Tyr Glu Phe Asp Val Ile Leu Ser Pro Glu Leu Lys Val Gln Met  
 385 390 395 400

Lys Thr Ile Gln Leu Lys Leu Glu Asn Ile Arg Ser Ile Phe Glu Asn  
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Gln Gln Ala Gly Phe Arg Asn Leu Ala Asp Lys His Val Arg Pro Ile  
 420 425 430

Gln Phe Val Val Pro Thr Pro Glu Asn Leu Val Thr Ser Gly Thr Pro  
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Leu Ser Ser Leu Glu Asn Cys Ala His Ala Pro Glu Arg Val Gly Pro  
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Cys Phe Leu Glu Arg Lys Asp Asp Phe Gln Met Tyr Ala Lys Tyr Cys  
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Gln Asn Lys Pro Arg Ser Glu Thr Ile Trp Arg Lys Tyr Ser Glu Cys  
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Asp Ser Tyr Leu Leu Lys Pro Val Gln Arg Ile Thr Lys Tyr Gln Leu  
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Asn Glu Leu Gly Lys Met Ile Met Gln Gly Gly Phe Ser Val Trp Ile  
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Gly His Lys Lys Gly Ala Thr Lys Met Lys Asp Leu Ala Arg Phe Lys  
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Pro Leu Met Arg Pro Val Ser Glu Met Ala Leu Leu Tyr  
915 920 925